

Docket No. CL001181DIV2
Serial No. To Be Assigned
Inventors: Ming-Hui WEI et al.
Title: ISOLATED HUMAN ENZYME PROTEINS...

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1 TGGAGGAGCC AGCGGAAGGA CGGTGTGCGG GCCGGCCAGC CCTGGACGAA
51 AGAAGAGGGC CCTCCAGGC CAGTCTGGGC ACCCTGGGAT AGCGGCTGCA
101 GCCAGGCATG GCCGACTCTG CACAGGCCCA GAAGCTGGTG TACCTGGTCA
151 CAGGGGGCTG TGGCTTCCTG GGAGAGCACG TGGTGCGAAT GCTGCTGCAG
201 CGGAGAGCCC GGCTCGGGGA GCTGCGGGTC TTTGACCAAC ACCTGGGTCC
251 CTGGCTGGAG GAGCTGAAGA CAGGTACCCG GAACGTGATC GAGGCTTGTG
301 TGCAGACCGG AACACGGTTC CTGGTCTACA CCAGCAGCAT GGAAGTTGTG
351 GGGCCTAACA CCAAAGGTCA CCCCTTCTAC AGGGGCAACG AAGACACCCC
401 ATACGAAGCA GTGCACAGGC ACCCCTATCC TTGCAGCAAG GCCCTGGCCG
451 AGTGGCTGGT CCTGGAGGCC AACGGGAGGA AGGTCCGTGG GGGGCTGCCC
501 CTGGTGACGT GTGCCCTTCG TCCCACGGGC ATCTACGGTG AAGGCCACCA
551 GATCATGAGG GACTTCTACC GCCAGGGCCT GCGCCTGGGA GGTGCGCTCT
601 TCCGGGCCAT CCCGGCCTCT GTGGAGCATG GCCGGGTCTA TGTGGGCAAT
651 GTTGCTTGGG TGCACGTGCT GGCAGCCCGG GAGCTGGAGC AGCGGGCAGC
701 CCTGATGGGC GGCCAGGTAT ACTTCTGCTA CGATGGATCA CCCTACAGGA
751 GCTACGAGGA TTTCAACATG GAGTTCCTGG GCCCCTGCGG ACTGCGGCTG
801 GTGGGCGCCC GCCCATTGCT GCCCTACTGG CTGCTGGTGT TCCTGGCTGC
851 CCTCAATGCC CTGCTGCAGT GGCTGCTGCG GCCACTGGTG CTCTACGCAC
901 CCTGTCTGAA CCCCTACACG CTGGCCGTGG CCAACACCAC CTTACCGTTC
951 AGCACCGACA AGGCTCAGCG CCATTTTCGG TATGAGCCCC TGTCTCTGTG
1001 GGAGGATAGC CGGACCCGCA CCATTCTCTG GGTACAGGCC GCTACGGGTT
1051 CAGCCCAGTG ACGGTGGGGC TGGGGCCTGG AGGCCCAGAT ACAGCACATC
1101 CACCAGAGTC CCGAGCCCTC ACACCCTGGA CGGGAAGGGA CAGCTGCATT
1151 CCAGAGCAGG AGGCAGGGCT CTGGGGCCAG AATGGCTGTC CTTGTCGTAG
1201 AGCCCTCCAC ATTTTCTTTT TCTTTTTTGA GACAGGCTCT TGCTCTGTCA
1251 CCCAGACTGG AGTGCAGTGG TGTGATCATA GCTCACTGCA CCCTCAACCT
1301 CCTGGGTTCA AGCAATCCTC CTGCCTCAGC CTCCTGAACA GCTGGGACCA
1351 CAGGTGCACG CCACCATAAC TGGCTTTTTT TTGTTGCTTT TAGAGACAGG
1401 GTCTCACTAT ATTGCTCAAG GCTGGACTTG AACTCCTGGG CTCAAGTGAT
1451 CTTCCACAGT GGGCCTCCCA AAACGCTGGA ACTACAAGTG TGAGCCACCG
1501 CGCCTGGCCC ACCGCCTCTC CACATTTTCA ATCCAGGAGC CTTGAGTCTG
1551 TGGCTGTGTC CTGACACCTC CAGAGTTCTG AGGGCCGTCA GGACACGGGA
1601 GGGTTTGGGG ACAGAGTGTC CTTCTCTGTG CCTATCATCA CCAGTCCTGA
1651 TGGCCGCTTG GTGAGTGTCT GGTGCCCTGG TGGCTTGCCC CAGCTCTCTT
1701 GTGGCTTTCT GAGCAGGAAG CGAGCACTAG GCTCCACAGG CTTACGCTGT
1751 GTCTCCTGCC AGCCACACAG CGACCCATCG GTGCAGAGTG CAGACGCGGG
1801 TGTGTTTCTT CCAGCCCACC TCAGTCCCTC TTTGGGAGGT GATGTTCCCA
1851 TTGTTTTTCA AAGGCCTCAC CTTCAACTGT TCTGTTTTAG AATTCCCCTC
1901 TGGAGGGCTA TGGCCTCCCT ATGGTTTCAC TTCCACCTA CTTCTACCTA
1951 AGTTCCTTCC CAGCACATCG CCAGCCCTGG GCCTGGGGAT GTCCCAATG
2001 CTGTACCTGG CTGACCCCGG ATTAAAAGCC TCATCCACGA AAAAAAAAAA
2051 AAAAAAAAAA AAAAAAAAAA A

```

(SEQ ID NO: 1)

FEATURES:

5'UTR: 1-107
Start Codon: 108
Stop Codon: 1059
3'UTR: 1062

HOMOLOGOUS PROTEINS:

Top 10 BLAST Hits:

| | | |
|--|-----|-------|
| CRA 335001098696094 /altid=gi 11545403 /def=gb AAG37824.1 AF277... | 638 | 0.0 |
| CRA 335001098696092 /altid=gi 11545401 /def=gb AAG37823.1 AF277... | 562 | e-159 |
| CRA 18000005106837 /altid=gi 2563999 /def=dbj BAA22931.1 (AB00... | 484 | e-136 |
| CRA 18000005043125 /altid=gi 9629084 /def=ref NP_044103.1 MC15... | 269 | 3e-71 |
| CRA 89000000192042 /altid=gi 9634716 /def=ref NP_039008.1 ORF ... | 257 | 2e-67 |
| CRA 18000004899504 /altid=gi 540666 /def=pir S41971 3beta-hydr... | 240 | 1e-62 |
| CRA 335001098644340 /altid=gi 11251676 /def=pir T37430 hydroxy... | 213 | 2e-54 |
| CRA 18000004942649 /altid=gi 112779 /def=sp P26670 3BHS_VACCV 3... | 212 | 4e-54 |

FIGURE 1A

Docket No. CL001181DIV2
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| | | | | | |
|--------------------|-------------------|----------------------|---------|-----|-------|
| CRA 18000004942648 | /altid=gi 9791111 | /def=ref NP_063838.1 | A44L... | 211 | 9e-54 |
| CRA 73000005493670 | /altid=gi 9634564 | /def=ref NP_038102.1 | TA55... | 211 | 9e-54 |

FIGURE 1B

Docket No. CL001181DIV2
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EST:

| | | |
|--|------|-------|
| gi 11283574 /dataset=dbest /taxon=96... | 1283 | 0.0 |
| gi 11643588 /dataset=dbest /taxon=96... | 1116 | 0.0 |
| gi 13134586 /dataset=dbest /taxon=960... | 527 | e-147 |
| gi 9334685 /dataset=dbest /taxon=960... | 462 | e-128 |

EXPRESSION INFORMATION FOR MODULATORY USE:

| | |
|-------------|--------|
| gi 11283574 | brain |
| gi 11643588 | kidney |
| gi 13134586 | colon |
| gi 9334685 | uterus |

FIGURE 1C

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1 MADSAQAQKL VYLVTTGGCGF LGEHVVRMLL QREPRLGELR VFDQHLGPWL
51 EELKTGTRNV IEACVQTGTR FLVYTSSMEV VGPNTKGHPF YRGNEPTPYE
101 AVHRHPYPCS KALAEWLVLE ANGRKVRGGL PLVTCALRPT GIYGEHQIM
151 RDFYRQGLRL GGWLFRAIPA SVEHGRVYVG NVAWMHVLAA RELEQRAALM
201 GGQVFCYDG SPYRSYEDFN MEFLGPCGLR LVGARPLLPY WLLVFLAALN
251 ALLQWLLRPL VLYAPLLNPY TLAVANTTFT VSTDKAQRHF GYEPLFSWED
301 SRRTRILWVQ AATGSAQ
(SEQ ID NO: 2)

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

276-279 NTTF

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

283-285 TDK

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 4

1 76-79 SSME
2 97-100 TPYE
3 215-218 SYED
4 297-300 SWED

[4] PDOC00007 PS00007 TYR_PHOSPHO_SITE
Tyrosine kinase phosphorylation site

92-99 RGNEDTPY

[5] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

157-162 GLRLGG

[6] PDOC00009 PS00009 AMIDATION
Amidation site

122-125 NGRK

[7] PDOC00029 PS00029 LEUCINE_ZIPPER
Leucine zipper pattern

246-267 LAALNALLQWLLRPLVLYAPLL

Membrane spanning structure and domains:

| Helix | Begin | End | Score | Certainty |
|-------|-------|-----|-------|-----------|
| 1 | 6 | 26 | 0.633 | Putative |
| 2 | 237 | 257 | 1.571 | Certain |
| 3 | 260 | 280 | 0.819 | Putative |

FIGURE 2A

Docket No. CL001181DIV2
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BLAST Alignment to Top Hit:

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>CRA|335001098696094 /altid=gi|11545403
      /def=gb|AAG37824.1|AF277719_1 (AF277719) 3
      beta-hydroxy-delta 5-C27-steroid oxidoreductase [Homo
      sapiens] /org=Homo sapiens /taxon=9606 /dataset=nraa
      /length=369
      Length = 369

Score = 638 bits (1627), Expect = 0.0
Identities = 315/369 (85%), Positives = 316/369 (85%), Gaps = 52/369 (14%)

Query: 1  MADSAQAQKLVLVTGGCGFLGEHVVRMLLQREPRLGELRVFDQHLGPWLEELKTG---- 56
      MADSAQAQKLVLVTGGCGFLGEHVVRMLLQREPRLGELRVFDQHLGPWLEELKTG
Sbjct: 1  MADSAQAQKLVLVTGGCGFLGEHVVRMLLQREPRLGELRVFDQHLGPWLEELKTGPVRV 60

Query: 57  -----TRNVIEACVQTG 68
      TRNVIEACVQTG
Sbjct: 61  TAIQGDVTQAHEVAAVAGAHVVIHTAGLVDVFGRASPKTIHEVNVQGTRNVIEACVQTG 120

Query: 69  TRFLVYTSSMEVVGPNTKGHPFYRGNEPTPYEAVHRHPYPCSKALAEWLVLLEANGRKVRG 128
      TRFLVYTSSMEVVGPNTKGHPFYRGNEPTPYEAVHRHPYPCSKALAEWLVLLEANGRKVRG
Sbjct: 121 TRFLVYTSSMEVVGPNTKGHPFYRGNEPTPYEAVHRHPYPCSKALAEWLVLLEANGRKVRG 180

Query: 129 GLPLVTCALRPTGIYGEGHQIMRDFYRQGLRLGGWLFRAIPASVEHGRVYVGNVAMMHVL 188
      GLPLVTCALRPTGIYGEGHQIMRDFYRQGLRLGGWLFRAIPASVEHGRVYVGNVAMMHVL
Sbjct: 181 GLPLVTCALRPTGIYGEGHQIMRDFYRQGLRLGGWLFRAIPASVEHGRVYVGNVAMMHVL 240

Query: 189 AARELEQRAALMGGQVYFCYDGSPPYRSYEDFNMEFLGPCGLRLVGARPLLPHYWLLVFLAA 248
      AARELEQRAALMGGQVYFCYDGSPPYRSYEDFNMEFLGPCGLRLVGARPLLPHYWLLVFLAA
Sbjct: 241 AARELEQRAALMGGQVYFCYDGSPPYRSYEDFNMEFLGPCGLRLVGARPLLPHYWLLVFLAA 300

Query: 249 LNALLQWLLRPLVLYAPLLNPYTLAVANTTFTVSTDKAQRHFGYEPLFSWEDSRTRTILW 308
      LNALLQWLLRPLVLYAPLLNPYTLAVANTTFTVSTDKAQRHFGYEPLFSWEDSRTRTILW
Sbjct: 301 LNALLQWLLRPLVLYAPLLNPYTLAVANATFTVSTDKAQRHFGYEPLFSWEDSRTRTILW 360

Query: 309 VQAATGSAQ 317
      VQAATGSAQ
Sbjct: 361 VQAATGSAQ 369 (SEQ ID NO: 4)
```

Hammer search results (Pfam):

Scores for sequence family classification (score includes all domains):

| Model | Description | Score | E-value | N |
|---------|--|-------|----------|---|
| PF01073 | 3-beta hydroxysteroid dehydrogenase/isomeras | 558.2 | 5.5e-164 | 2 |
| PF01370 | NAD dependent epimerase/dehydratase family | 13.3 | 0.005 | 1 |
| PF00438 | S-adenosylmethionine synthetase | 1.8 | 0.78 | 1 |

Parsed for domains:

| Model | Domain | seq-f | seq-t | hmm-f | hmm-t | score | E-value |
|---------|--------|-------|--------|-------|--------|-------|----------|
| PF01370 | 1/1 | 12 | 31 .. | 1 | 20 [. | 13.3 | 0.005 |
| PF01073 | 1/2 | 1 | 52 [. | 1 | 53 [. | 69.6 | 3.9e-18 |
| PF00438 | 1/1 | 289 | 299 .. | 365 | 376 .] | 1.8 | 0.78 |
| PF01073 | 2/2 | 55 | 313 .. | 159 | 425 .] | 489.6 | 2.4e-143 |

FIGURE 2B

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1  ATTTGCATTA GCCGGTGGCA GCCAACAGGT GCCTGTTTTG GAGAGAGGTC
51 CAGGGAGGAG AGATGAGCAG GGTGCCGTTG GTGACATGGC CAGTCATTTC
101 AGGAGCTGCC CCAACCCAG ACTTGCCCA GCAGTCCGGG ACCCCACTGT
151 GACCAGGCAG ATGCTCGAAG GAGTCAGTGG CTCTCTTACC CAGTGCAGAT
201 TTCCCTGGAG TTCCCTGCGG GTGACTTAGA ATGGCCACCA GAGGCTTAGG
251 ATGCTGCCCC AAAGAGGGAG GGCTCCTGGA AGCAGAGTCG AGAGAGTCAG
301 TGCCGGGTTA GCGGGAGCTG GAGGCAGAGC TGCAGCTCCA GGCCTGGTGG
351 GCGTGGACCT GGGGTGCTGG CTGGCAGGCG TGCTCAGGGG CAGGAAGTGG
401 GGGACTCTTC CCTGACCATC GCATCTCACC CTGGCAGATG GTGGCCGACA
451 TGCGGGAGAA GCGCTACGTG CAGGAGGGCA TTGGCAGCAG CTACCTGTTC
501 CGGGTGGACC ACGACACCAT CATCGATGCC ACCAAGTGTG GCAACCTGGC
551 CAGATTTCATC AACCACTGCT GCACGGTGGC CCAGGGGGCA GCGGGGGCAG
601 GAGTTGGGGG TCGGTGGGGG TGGCCACGGC TCACACGCCC TTCCATCCGC
651 AGCCTAAGTG CTACGCCAAG GTCATCACC TCGAGTCCCA GAAGAAGATC
701 GTGATCTACT CCAAGCAGCC CATTGGCGTG GACGAGGAGA TCACCTACGA
751 CTACAAGTTC CCACTGGAAG ACAACAAGAT CCCGTGTCTG TGTGGCACAG
801 AGAGCTGCCG GGGCTCCCTA AACTGAGGTG GGGCAGGATG GGTGCCACA
851 CCCCTATTTA TTCCCTCTGG TGCCCTGAGC TCCCAGCACC CCCCCAGCCT
901 TAGTGGGCTC AGCAGGGCCC ACATGCCCC ATCTCCAAGC GTGGGGTTGG
951 GGGCCCCAAG CCCAGCGAGG GAGCCTCAGT CCCTGGAGGC AGCTTCTGCC
1001 TCTCCTGTCG CCCCTGCCCA CCACCCCTG ATTGTTTTTC TTTGCGGAGA
1051 AGAAGCTGTA AATGTTTTGT AGCAGCCAGC AGCTGTTTCC TGTGGAAACC
1101 TGGGGTGCCG GCCTGTACAG ATTCTGTCTT GGGGGGCTAC ACAGTCTCTT
1151 CGCTTTGTGT TAATGGGGAC TTCCCTTTAC GCCCTGCGTG TACCCCTCCC
1201 CAGTTTAGGG GTCTCTGGGG CAGTGGCCAT GTTCTCCCC TGGGGGGGCT
1251 CTGCACCCCC AGTCTGGGG ACTCCGTGCC TGGAAACCTG CCTCATCTGT
1301 TCCTGCCAGA CCCTGAGGGT CACCCTTECA CCCTGGTGTG ACTCCCCGGC
1351 TCAGCCAGGC CAGGATGGCG GGGTGGGTCC CTTTGTCTGG GCTGGACTGT
1401 ACATATGTTA ATAGCGCAAA CCCGACGCCA CATTTTTATA ATTGTGATTA
1451 AACTTTATTG TACAAAAGTG TTTGGTGGT GTATTTGGGC AGGAGCGAGG
1501 GGTGGGGGTG AGAGGGCAGC GAGGGTTGTG CAAGTTGAAG AGAGGGAAAA
1551 GTGGGTACCT GAAGTGTGGG GCAGGTAAAG GGGCCTTCAG GCAAGAGCCC
1601 AGACCTGCAG AGACAGTCCG AGACTGTCTC GGACCCCTG ACAGGCTGCA
1651 GCAGCCGCAC CCGCACCAGG AATACCCAC CAGTGCCCGC CAGGGTGGTG
1701 CCAAGGTCAG GCCTCCCCTT CCTACAATCA CAGCTGCAGC TGGACCTCCG
1751 GCCTCCTGGG AAGCCAGCA GGAGGGAAGG CCTGAGGTCA CACTGTGGGA
1801 TGAGGTCACC GCTGGCTCCA CCCACAGCCC CAGACCCCTT CAGCCCCTC
1851 TGCAAGTTCG AGCTTCATCC CCACCAAGTT CTCCGCTGGA CCCAGATGCC
1901 AGTGGAGCAC AGAGCGGCCG CCAGGGGGCG CCTTGGGGCA AGAGTGGTGG
1951 GGGTTGTGGC TGGGCGGGTC TCTGTTCTTG GAATGGGGCA GGAGGGAGAA
2001 GGAGGAGCCA GCGGAAGGAC GGTGTGCGGG CCGGCCAGCC CTGGACGAAA
2051 GAAGAGGGCC CCTCCAGGCC AGTCTGGGCA CCCTGGGATA GCGGCTGCAG
2101 GTAGGCAGAG GCGCTGCCAG TGCCCAGGTG GCCTTTCCCT CCATCCGGCC
2151 CTTCCACCTT TCCTATAACC TTCCCTCCAC CTCCCTCAAC TCCTGGCCTC
2201 CCCACCCCTT TACTGCCTTC AAATCTCTCT CCCTAAACCC TGACCCCTTC
2251 CTGCACCCCA AGCCCGCCCC TCTCTCCGTA ACTCAGCCAT CAGCAGGGGC
2301 AGACGGCAGG TGGCCTGGTT GCTGCAGCTC CCAGGATCAG CTCTGCCCTC
2351 CCGCCAAACG CCAGCCTCGT CACCGCTCCA GGGCACCTCC AGCAGTAACA
2401 GGTGTTTGCA GCAGGTGGCA GCCAGCCCCT GGATGAGCCA AGGTCTCTTC
2451 CCCAGCCAGG CATGGCCGAC TCTGCACAGG CCCAGAAGCT GGTGTACCTG
2501 GTCACAGGGG GCTGTGGCTT CCTGGGAGAG CACGTGGTGC GAATGCTGCT
2551 GCAGCGGGAG CCCCAGCTCG GGGAGCTGCG GGTCTTTGAC CAACACCTGG
2601 GTCCCTGGCT GGAGGAGCTG AAGACAGGTT CTTGTTGGGG GAGCTTGTGG
2651 TGGAGAGGGT GTGGACGCTT CCCCAACCCT TCCCAAGCTG GGATCCCCAC
2701 CCCTGCAGTG GAACAGATGA TGCTGGTTTC TGTCCACATG GATGGGTGCA
2751 GTGAGTCACA TTGGGAACGT GACTCCAGGG TGGAAAGATG ACCCAGCCTC
2801 TGGCCTCTGG CCCCAGCTCT GACATGGCCT GTGTCCTCCA ACCCCGGCCA
2851 GGGCCTGTGA GGGTGAAGTC CATCCAGGGG GACGTGACCC AGGCCATGA
2901 GGTGGCAGCA GCTGTGGCCG GAGCCCATGT GGTCTATCCAC ACGGCTGGGC
2951 TGGTAGACGT GTTTGGCAGG GCCAGTCCCA AGACCATCCA TGAGGTCAAC
3001 GTGCAGGGTG AGGAGCTCTG GACACTCCTG GCCATCTTGC CTGTTTGTTC
3051 CCCACTCTGT CTTTGGCCTT GACCTCCGGT GACTCCCTG GGACAAGTTG

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FIGURE 3A

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| | | | | | |
|------|------------|------------|------------|------------|------------|
| 3101 | TCCTATTGAC | AGCCCTGCC | CCGCCTCCCC | TGACCTGTCA | TGGTTTTCCC |
| 3151 | TGGACCTGGG | ATGGGGAGGA | GGAAGATGCA | GAGAGGGAAG | AAGCTGCAGC |
| 3201 | TTGGATACGC | CTCCTCCTCT | GCCAGGTACC | CGGAACGTGA | TCGAGGCTTG |
| 3251 | TGTGCAGACC | GGAACACGGT | TCCTGGTCTA | CACCAGCAGC | ATGGAAGTTG |
| 3301 | TGGGGCCTAA | CACCAAAGGT | CACCCCTTCT | ACAGGTGAGT | GGCAGGCCCT |
| 3351 | CTTGTCTCT | AAGAGCCCAT | TTCCTCAGC | ATTGAGTCTT | CCTTCTCCTC |
| 3401 | CCACCAGGGG | CAACGAAGAC | ACCCCATACG | AAGCAGTGCA | CAGGCACCCC |
| 3451 | TATCCTTGCA | GCAAGGCCCT | GGCCGAGTGG | CTGGTCCTGG | AGGCCAACGG |
| 3501 | GAGGAAGGTG | AGCCCAAGAA | AAGGAGGCGC | AGAGATGGGG | CTCCTGCCCT |
| 3551 | GCACACCCCC | TTACCCTGCC | AGCCCAAGGA | GGCCGGGGCC | GAGAGCAAGC |
| 3601 | TGTGGGTGCC | CAGGTCTCAG | CAGTACCTGC | CTTTGCCACC | AGGTCCGTGG |
| 3651 | GGGGCTGCC | CTGGTGACGT | GTGCCCTTCG | TCCACAGGGC | ATCTACGGTG |
| 3701 | AAGGCCACCA | GATCATGAGG | GACTTCTACC | GCCAGGGCCT | GCGCCTGGGA |
| 3751 | GTTTGGCTCT | TCCGGGCCAT | CCCGCCTCT | GTGGAGCATG | GCCGGGTCTA |
| 3801 | TGTGGGTGAG | GACTGGGCTA | GGCAGGGGGA | GGCTGAGAAT | ATGGCAGGAG |
| 3851 | GACTTGCTCT | AGAAGGGGGC | AGGACCCACA | TGGCCCTGGG | AGAGAAGTGT |
| 3901 | GGACTCTGGC | TAGAAAAATA | TGGTCTATAC | ATGGGCCAAG | GTAGACTGTG |
| 3951 | ATTATGTCTC | CACAGCCTGC | AGAGAATACA | GGATCCATGC | AAGTTGGGAC |
| 4001 | ATTAAAAAGT | GTATCATAGG | CTACAGAGAA | GATTGCAGCT | ATGGGAGCAG |
| 4051 | CCATTCCCCA | GGAGAGGGAG | GGAGAGGGAC | AGTGTGTACA | CAGCACTAAA |
| 4101 | AGGGCTGGGT | TCAGTGGCTC | GCATCTATAA | TCCAGCACT | TTAGGAGGCT |
| 4151 | GAGGCGGGAG | GATGGCCTGA | GCCCAGGAGT | TGGAGGCTGC | AGTGAGCTAT |
| 4201 | GACCGCACCA | CTGCACTCCA | GCCTGGATGA | CAGAGACAGA | CCCTGTCTCT |
| 4251 | AAAACTTTTT | TTAAAGGAAG | TAGCATCTAC | ACAGGGAATA | AGGTCACCTG |
| 4301 | CCACTCCATC | CTGCAGTCCC | CAAGCCTCTC | AGGGCCCACC | ACGCAGGTCC |
| 4351 | TGGTTTCTCT | ATCCTCTCCC | CAGGTTCTTT | GCAGATGCAG | GCTGGGCCAG |
| 4401 | GAGAGCAAGT | GACTACCAGG | GCGAGGGAGA | AGGCAGCCTT | TCCCAGGCTG |
| 4451 | CTGTGGGGAT | GTGGGCGGCA | ACTACCTGGG | CCCAAAGAGG | GGGTGGCCCA |
| 4501 | GGAGAGCAGC | CTCGATGTGG | TGTTGCAAGG | GCACTCAGGG | GTGTGTCCGC |
| 4551 | CTCTCTTCCG | CCACCGGCAG | GCAATGTTGC | CTGGATGCAC | GTGCTGGCAG |
| 4601 | CCCGGGAGCT | GGAGCAGCGG | GCAGCCCTGA | TGGGCGGCCA | GGTATACTTC |
| 4651 | TGCTACGATG | GATCACCTTA | CAGGAGCTAC | GAGGATTTC | ACATGGAGTT |
| 4701 | CCTGGGCCCC | TGCGGACTGC | GGCTGGTGGG | CGCCCGCCCA | TTGCTGCCCT |
| 4751 | ACTGGCTGCT | GGTGTTCCTG | GCTGCCCTCA | ATGCCCTGCT | GCAGTGGCTG |
| 4801 | CTGCGGCCAC | TGGTGTCTTA | CGCACCCCTG | CTGAACCCCT | ACACGCTGGC |
| 4851 | CGTGGCCAA | ACCACCTTCA | CCGTACAGAC | CGACAAGGCT | CAGCGCCATT |
| 4901 | TCGGCTATGA | GCCCCGTTC | TCGTGGGAGG | ATAGCCGGAC | CCGCACCATT |
| 4951 | CTCTGGGTAC | AGGCCGCTAC | GGGTTAGGCC | CAGTGACGGT | GGGGCTGGGG |
| 5001 | CCTGGAGGCC | CAGATACAGC | ACATCCACCC | AGGTCCCAG | CCCTCACACC |
| 5051 | CTGGACGGGA | AGGGACAGCT | GCATTCCAGA | GCAGGAGGCA | GGGCTTCTGG |
| 5101 | GGCCAGAATG | GCTGTCTTGG | TCGTAGAGCC | CTCCACATTT | TCTTTTTCTT |
| 5151 | TTTTGAGACA | GGGTCTTGCT | CTGTACCCCA | GACTGGAGTG | CAGTGGTGTG |
| 5201 | ATCATAGCTC | ATGCAACCCT | CAACCTCCTG | GTTTCAAGCA | ATCCTCCTGC |
| 5251 | CTCAGCCTCC | TTGAACAGCT | GGGACCACAG | GTGCACGCCA | CCACACCTGG |
| 5301 | CTTTTTTTTG | TTGTTTTTAG | AGACAGGGTC | TCACTATATT | GCTCAGGCTG |
| 5351 | GTCTTGAAC | CCTGGGCTCA | AGTGATCTTC | CCACGTGGGC | CTCCAAAAC |
| 5401 | GCTGGAAC | CAAGTGTGAG | CCACCGCGCC | TGGCCCAAGC | CCTCCACATT |
| 5451 | TTCAATCCAG | GAGCCTTGAG | TCTGTGTTGT | GTCCTGACAC | CTCCAAGTTC |
| 5501 | TAGGGCCGTC | AGGACACGGG | AGGGTTTGGG | GACAGAGTGT | CCTTCTCTG |
| 5551 | TCCTCTCATC | CCAGTCCTGA | TGGCCGCTTG | GTGAGTGTCT | GGTGCCCTGG |
| 5601 | TGGCCTGCCC | CAGCTCTCTT | CTGGCTTTCT | GAGCAGGAAG | CGAGCAGAGG |
| 5651 | CTCCACAGGC | TTACGCTGCT | CTCCTGACAG | CCACACGCGA | CCCTCGGTGC |
| 5701 | AGAGTGACAG | GGCGGTCTTG | GTTCTCCAG | CCACCTCAGT | CCCTCTTTGG |
| 5751 | GAGGTGATGT | TCCCATTGTT | TTTCAAAGGC | CTACCTTCA | ACTGTCTGTC |
| 5801 | TTAGAATTCC | CCTCTGGAGG | GCTATGGCCT | CCCTATGCTT | TCATTCCCA |
| 5851 | CCTCTCTACC | TAAGTTCCTT | CCCAGCACAT | CGCCAGCCCT | GGGCCTGGGG |
| 5901 | ATGTCCCCAA | TGCTGTACCT | GGCTGACCCC | GGATTAAAAG | CCTCATCCAC |
| 5951 | GACCGTGTCC | ATCTGTCTGT | CCAGCTCTCC | CTCCCATCCC | CCCACCCCAT |
| 6001 | GTCCGCCTCC | CCACGCGGCC | CATCCACAGT | GGGGACAGAA | GGAAGTGAGC |
| 6051 | ACACGGCACA | CCCGCTGTTG | GATTGGTTGC | TATTTCTCCC | GTCCACAGG |
| 6101 | GCCTGACCTG | GCCCAGGGTG | GGGTGGGGGG | CTCTGGGGAC | AGGACATGCA |
| 6151 | GGGAGGAAGG | GGGGGACAGG | ATTTTCCTGT | GTTTATCCA | TTTGCAAGTT |

FIGURE 3B

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6201 GGTACCAAT AGAAATGGGA CTCTGAGGGC TAACAGAAAT GGGACTCTGA
6251 GGGCTAACAG GAGAGGGCGG CCTGGCTCTG GGGCCAGCC AGGCCCCAGG
6301 AGTCCTGTCC CCTCTGAGAA GGGGAGGGAG AGAGCTCTAG AAACCAACGG
6351 AGAAACAGAG AAGGGGGCAG GGGCTCATGT CAGCAAACAC GGCTACATCA
6401 CGTGACACGC CAGTGACACA GAAACACACG CCAACGCACA CGGCTGCACA
6451 GCGGGCAGGG GCGGTTAGGG GAAAGGGAGC CGGGGCCACC CATCTTGTC
6501 TCTGCAGGGC GGGCTGGGGG GCAGGGTGAA TGCATAGAAC ACATCATGTG
6551 TACACGCTCA GGGCGTGCCA AGAGCGTGCG TCGACCCACG GGTACATGGG
6601 ATGGACACGC AGTGTGCTTC ATGAGGGGTG GGAACAGGGA GGAGGGGGAA
6651 GAGGAAGCAC TGAGCCCTGG CCAGGCCCCG GACCACCCGC AGGGCACACG
6701 TGGGGCACAT GTGGGCTCAA TGGTTGCAGG CGCCTGGGCA GGTAGCACAC
6751 ATTTGTCCAA GAACATGCAA AAGACACCAG CCTCCAGACA ACATGCCAGG
6801 ACGCACACAG ACAGCAGCCA ACAAGCAGGC ACATCATAGG ATGTGGAGGA
6851 CGCATAGAAA GGGCACAGCA GACCCTTAGA GATCCCCTGG TCCACCTGAG
6901 GCCCAGAGAT GGGCAGCTGT GGGCCCAATG CCACTCCAGG TGGGGGGAGT
6951 GGTGCCCCAG CCACTGCTCA ACCCTTCTCC TGTGGCCCCA AGGCCGTGGG
7001 ACTTCCGGAA ACACCTGGGC TGAATGGGGG TCCTGTCCAG GCGGCCGGAA
7051 GAGGGGACTG GGGGCTGGGG CTTGCTCTGA TGTCTCCCAA GCAGCCCAGG
7101 ATGGGAGCAG GAGGGCCGTG GCCAGACTTG GGGCAGACTT CCTGTCCTGC
7151 AGAGGGGCGT TCTGGGAAGG GACAGGCAGG CCCCAGCTC AGGACAGCCC
7201 ACCTGGGGTT ACGCACGTGG CCACACTGAC ACACACACAG GACAAGGGAG
7251 AGCTCGGCTG TCTGAGCTCG GGTAGAGGTG GAGGGGTACT GTGTTCTGGG
7301 A

```

(SEQ ID NO: 3)

FEATURES:

Start: 2462
Exon: 2462-2627
Intron: 2628-3225
Exon: 3226-3334
Intron: 3335-3407
Exon: 3408-3507
Intron: 3508-3642
Exon: 3643-3805
Intron: 3806-4570
Exon: 4571-4983
Stop: 4984

SNPs:

| DNA Position | Major | Minor | Domain | Protein Position | Major | Minor |
|-----------------|-------|-------|----------------|---------------------|-------|-------|
| 1010 | A | G | Beyond ORF(5') | | | |
| 1151 | C | T | Beyond ORF(5') | | | |
| 4805 | G | A | Exon | 258 | R | Q |
| 6293 | G | A | Beyond ORF(3') | | | |

Context:

DNA
Position

```

1010 TCCAAGCAGCCCATTTGGCGTGGACGAGGAGATCACCTACGACTACAAGTTCCCACTGGAA
GACAAACAAGATCCCGTGTCTGTGTGGCACAGAGAGCTGCCGGGGCTCCCTAAACTGAGGT
GGGGCAGGATGGGTGCCACACCCCTATTTATTTCCCCTGGTGCCTGAGCTCCCAGCAC
CCCCCAGCCTTAGTGGGCTCAGCAGGGCCACATGCCCCATCTCCAAGCGTGGGGTTG
GGGGCCCAAGCCAGCGAGGGAGCCTCAGTCCCTGGAGGCAGCTTCTGCCTCTCCTGTC
[A,G]
CCCCTGCCCCACCACCCCTGATTGTTTTTCTTTGCGGAGAAGAAGCTGTAAATGTTTTGT
AGCAGCCAGCAGCTGTTTCTGTGGAAACCTGGGGTGCCGGCTGTACAGATTCTGTCT

```

FIGURE 3C

Docket No. CL001181DIV2
Serial No. To Be Assigned
Inventors: Ming-Hui WEI et al.
Title: ISOLATED HUMAN ENZYME PROTEINS...

GGGGGGCTACACAGTCCTCTCGCTTTGTGTTAATGGGGACTTCCCCCTTACGCCCTGCGTG
TACCCCTCCCCAGTTTAGGGGTCTCTGGGGCAGTGGCCATGTTCTCCCCCTGGGGGGGCT
CTGCACCCCCAGTCCTGGGGACTCCGTGCTGGAACCTGCCTCATCTGTTCTGCCAGA

1151 CCCCTATTTATTTCCCCCTGGTGCCCTGAGCTCCCAGCACCCCCCAGCCTTAGTGGGCTC
AGCAGGGCCCATGCCCCCATCTCCAAGCGTGGGGTGGGGGGCCCAAGCCAGCGAGG
GAGCCTCAGTCCCTGGAGGCAGCTTCTGCCTCTCCTGTGCCCCCTGCCACCACCCCTG
ATTGTTTTTCTTTGCGGAGAAGAAGCTGTAAATGTTTTGTAGCAGCCAGCAGCTGTTCC
TGTGGAAACCTGGGGTGCCGGCCTGTACAGATTCTGTCTGGGGGGCTACACAGTCCTCT
[C, T]
GCTTTGTGTTAATGGGGACTTCCCCCTTACGCCCTGCGTGTACCCCTCCCCAGTTTAGGGG
TCTCTGGGGCAGTGGCCATGTTCTCCCCCTGGGGGGGCTCTGCACCCCAAGTCTCGGGG
CTCCGTGCCTGGAACCTGCCTCATCTGTTCTGCCAGACCCTGAGGGTACCCTTCCAC
CCTGGTGTACTCCCCGGCTCAGCCAGGCCAGGATGGCGGGTGGGTCCCTTTTGCTGGG
CTGGACTGTACATATGTTAATAGCGCAAACCCGACGCCACATTTTATAATTGTGATTAA

4805 AGCAGCCTCGATGTGGTGTGCAAGGGCACTCAGGGGTGTGTCCGCCTCTCTTCCGCCAC
CGCAGGCAATGTTGCCTGGATGCACGTGCTGGCAGCCCGGGAGCTGGAGCAGCGGGCAG
CCCTGATGGGCGGCCAGGTATACTTCTGCTACGATGGATCACCTACAGGAGCTACGAGG
ATTTCAACATGGAGTTCTTGGGCCCCCTGCGGACTGCGGTGGTGGGCGCCCGCCATTGC
TGCCCTACTGGCTGCTGGTGTCTCTGGCTGCCCTCAATGCCCTGCTGCAGTGGCTGCTGC
[G, A]
GCCACTGGTGTCTTACGCACCCCTGCTGAACCCCTACACGCTGGCCGTGGCCAACACCAC
CTTCACCGTCAGCACCGACAAGGCTCAGCGCCATTTCTGGCTATGAGCCCTGTTCTCGTG
GGAGGATAGCCGGACCCGACCATTTCTCTGGGTACAGGCCGCTACGGGTTCAGCCCACTG
ACGGTGGGGCTGGGGCCTGGAGGCCAGATACAGCACATCCACCCAGGTCCCGAGCCCTC
ACACCCCTGGACGGGAAGGGACAGCTGCATTCAGAGCAGGAGGCAGGGCTTCTGGGGCCA

6293 CACCCCATGTCCGCCTCCCCACGGCGCCCATCCCACGTGGGGACAGAAGGAAGTGAGCAC
ACGCACACCCGCTGTTGGATTGGTTGCTATTTCTCCCGTCCCACAGGGCCTGACCTGGC
CCAGGGTGGGGTGGGGGGCTCTGGGGACAGGACATGCAGGGAGGAAGGGGGGGCAGGAT
TTTCTGTGTTTTATCCATTGCAAGTTGGTCACCAATAGAAATGGGACTCTGAGGGCTA
ACAGAAATGGGACTCTGAGGGCTAACAGGAGAGGGCGGCCTGGCTCTGGGCCCCAGCCAG
[G, A]
CCCCAGGAGTCTGTCCCCTCTGAGAAGGGGAGGGAGAGAGCTCTAGAAACCAACGGAGA
AACAGAGAAGGGGGCAGGGGCTCATGTCAGCAAACACGGCTACATCACGTGACACGCCAG
TGACACAGAAACACACGCCAACGCACACGGCTGCACAGCGGGCAGGGGCGGTTAGGGGAA
AGGGAGCCGGGGCCACCATCTTGTCTCTGCAGGGCGGGCTGGGGGGCAGGGTGAATGC
ATAGAACACATCATGTGTACACGCTCAGGGCGTGGCAAGAGCGTGCCTCGACCCACGGGT

Chromosome map:
Chromosome 12